

Sub A1

SEQUENCE PROTOCOL

<110> Degussa-Hüls AG

5/ <120> New nucleotide sequences coding for the ptsH gene

<130> 990219 BT

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 480

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (163) .. (429)

<223> ptsH wild-type gene

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ggacattgtt tttgcttccg gtaacgtggc aaaacgaaca atgtctcact agactaaagt 60

gagatcgaca ttaaattcccc tcccttgggg ggtttaacta acaaatcgct gcgccctaata 120

ccgttcggat taacggcgta gcaacacgaa aggacacttt cc atg gct tcc aag 174
Met Ala Ser Lys
1

act gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc 222
Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser
5 10 15 20

atc atc gct gaa gcg gct gct gag tac gac gac gaa atc ttg ctg acc 270
Ile Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu Ile Leu Leu Thr
25 30 35

ctg gtt ggc tcc gat gat gac gaa gag acc gac gcg tcc tct tcc ctc 318
Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala Ser Ser Ser Leu
40 45 50

atg atc atg gcg ctg ggc gca gag cac ggc aac gaa gtt acc gtc acc 366
Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu Val Thr Val Thr
55 60 65

tcc gac aac gct gaa gct gtt gag aag atc gct gcg ctt atc gca cag 414
Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala Leu Ile Ala Gln
70 75 80

gac ctt gac gct gag taaacaacgc tctgcttggt aaaagctcgt tagaagcttg 469
Asp Leu Asp Ala Glu
85

ttaaaagcgg t 480

$\langle 210 \rangle$	2
$\langle 211 \rangle$	89

Sub A1

<213> *Corynebacterium glutamicum*

5 / Met Ala Ser Lys Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala
1 5 10 15

Arg Pro Ala Ser Ile Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu
20 25 30

Ile Leu Leu Thr Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala
35 40 45

15 Ser Ser Ser Leu Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu
50 55 60

Val	Thr	Val	Thr	Ser	Asp	Asn	Ala	Glu	Ala	Val	Glu	Lys	Ile	Ala	Ala
65					70					75					80

20 Leu Ile Ala Gln Asp / Leu Asp Ala Glu
85

25 $\langle 211 \rangle$ 480

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

30 <221> CDS

$\langle 222 \rangle$ (163) .. (429)

<223> ptsH allele

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gagatcgaca ttaaattccc tcccttgggg ggtttaacta acaaatcgct gcgccctaata 120

40 ccgttcggat taacggcgta gcaacacgaa / aggacacttt cc atg gct tcc aag 174
Met Ala Ser Lys
1

act gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc 222
Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser
45 5 10 15 20

atc atc gct gaa acg gct gct gag tac ~~gac~~ gac gaa atc ttg ctg acc 270
Ile Ile Ala Glu Ala Ala Ala Glu Tyr ~~Asp~~ Asp Glu Ile Leu Leu Thr
25 30 35

ctg	gtt	ggc	tcc	gat	gat	gac	gaa	gag	acc	gac	gcg	tcc	tct	tcc	ctc	318
Leu	Val	Gly	Ser	Asp	Asp	Asp	Glu	Glu	Thr	Asp	Ala	Ser	Ser	Ser	Leu	
			40					45					50			

55 atg atc atg gcg ctg ggc gca gag cac ggc aac gaa gtt acc gtc acc 366
Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu Val Thr Val Thr

55 60 65

tcc gac aac gct gaa gct gtt gag aag atc gct gcg ctt atc gca cag 414
60 Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala Leu Ile Ala Gln
70 75 80

gac ctt gac gct gag taaacaacgc tctgcttggt aaaagctcgt taqaagcttg 469

Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)
Algeria	1980	12.5	4.5	36	100	100	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	1985	13.5	5.5	41	110	110	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	1990	14.5	6.5	45	120	120	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	1995	15.5	7.5	48	130	130	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2000	16.5	8.5	52	140	140	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2005	17.5	9.5	54	150	150	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2010	18.5	10.5	57	160	160	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2015	19.5	11.5	59	170	170	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2020	20.5	12.5	61	180	180	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2025	21.5	13.5	63	190	190	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2030	22.5	14.5	64	200	200	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2035	23.5	15.5	66	210	210	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2040	24.5	16.5	67	220	220	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2045	25.5	17.5	69	230	230	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2050	26.5	18.5	70	240	240	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2055	27.5	19.5	71	250	250	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2060	28.5	20.5	72	260	260	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2065	29.5	21.5	73	270	270	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2070	30.5	22.5	74	280	280	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2075	31.5	23.5	75	290	290	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2080	32.5	24.5	76	300	300	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2085	33.5	25.5	76	310	310	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2090	34.5	26.5	77	320	320	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2095	35.5	27.5	78	330	330	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2100	36.5	28.5	78	340	340	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2105	37.5	29.5	79	350	350	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2110	38.5	30.5	79	360	360	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2115	39.5	31.5	80	370	370	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2120	40.5	32.5	80	380	380	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2125	41.5	33.5	81	390	390	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2130	42.5	34.5	81	400	400	1.5	1.5	1.5	1.5	1.5	1.5
Algeria	2135	43.5	35.5									

SubA1

Asp Leu Asp Ala Glu
85

ttaaaagcgg t

480

<210> 4

<211> 89

<212> PRT

<213> Corynebacterium glutamicum

<400> 4

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1 5 10 15Arg Pro Ala Ser Ile Ile Ala Glu Thr Ala Ala Glu Tyr Asp Asp Glu
20 25 30Ile Leu Leu Thr Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala
35 40 45Ser Ser Ser Leu Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu
50 55 60Val Thr Val Thr Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala
65 70 75 80Leu Ile Ala Gln Asp Leu Asp Ala Glu
85

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<212> DNA

<213> Corynebacterium glutamicum

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<223> Primer ptsHexpl

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<212> DNA

<213> Corynebacterium glutamicum

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<223> Primer ptsHexp2

<400> 6

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20

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